F ig. 1

	AGG		TTA	ACTG CTAC AAAA	ACCA	GG A	AAAG	GACA	C AT	TCGA	CAAC	AGG	AAAG	T AA GAG		- 96 - 46 - 1
	ATG Me t	GGA GI y	AAC As n	AAC As n	TGT Cys	TAC Tyr	AAC As n	GTG Val	GTG Val	GTC Val	ATT	GTG Val	CTG Leu	CTG Leu	CTA Leu	45
				GAG GI u												90
				GGT GI y				Ar g		Туг						135
	AGC Ser	TGC	CCT Pr o	CCA Pr o	AGT Ser	ACC Thr	TTC Phe	TCC	AGC	ATA	GGT Gly	GGA Gly	CAG Gl ը	CCG Pro	AAC As n	180
		•							H4	⊢1BB	FII					
<u></u>	TGT Cys	AAC As n	ATC	TGC Cys	AGA Ar g	GTG Val	TGT Cys	GCA Al a	GGC	TAT	TTC	AGG Ar g	TTC Phe	AAG Lys	AAG Lys	225
	TTT	TGC Cys	TCC Ser	TCT Ser	ACC Thr	CAC Hi s	AAC As n	GCG Al a	GAG GI u	TGT Cys	GAG GI u	TGC Cys	ATT	GAA GI u	GGA GI y	270
				TTG Leu												315
	AGG Ar g	CCT Pro	GGC GI y	CAG GI n	GAG GI u	CTA Leu	ACG Thr	AAG Lys	CAG Gl n	GGT GI y	Çγs	AAA Lys H4-11	Thr	Cys	AGC Ser	360
Щ.																
in in the	Leu	GGA GI y	ACA Thr	Phe	AAT As n	As p	CAG Gl n	AAC As n	GGT GI y	ACT Thr	GGC GI y	GT C Val	TGT Cys	CGA Ar g	CCC Pro	405
1	TCC	ACC	AAC				CAC	CCA	ACC	TOT	CTC	CTT	440	400	000	450
-	Trp	Thr	Asn	TGC Cys	Ser	Leu	As p	GI y	AGG Ar g	Ser	Val	Leu	Lys	Thr	GGG GI y	450
	ACC Thr	ACG Thr	GAG GI u	AAG Lys	GAC As p	GTG Val	GTG Val	TGT Cys	GGA GI y	CCC Pr o	CCT Pro	GTG Val	GTG Val	AGC Ser	TTC Phe	495
								•								
				ACC Thr												540
	Ser GGG	Pr o	Ser		Thr	GTC	Ser	Val	Thr	O 19	GI u	GI y GCG	GI y CTG	Pr o	GI y	540 585
	Ser GGG GI y GCT	CAC Hi s	TCC Ser	Thr	Thr CAG GI n GCC	GTC Val	CTT Leu ATC	ACC Thr	Thr TTG Leu ATT	TTC Phe	CTG Leu	GCG AL a	GI y CTG Leu	ACA Thr	TCG Ser	
	GGG GI y GCT AI a CTC	CAC His	TCC Ser CTG Leu	Thr TTG Leu CTG	CAG GI n GCC AI a	GTC Val CTG Leu	CTT Leu ATC II e	ACC Thr TTC Phe	Thr TTG Leu ATT 11 e	TTC Phe ACT Thr	CTG Leu CTC Leu	GI y GCG AI a CTG Leu	CTG Leu TTC Phe	ACA Thr TCT Ser	TCG Ser GTG Val	585

Fig.1 (cont'd)

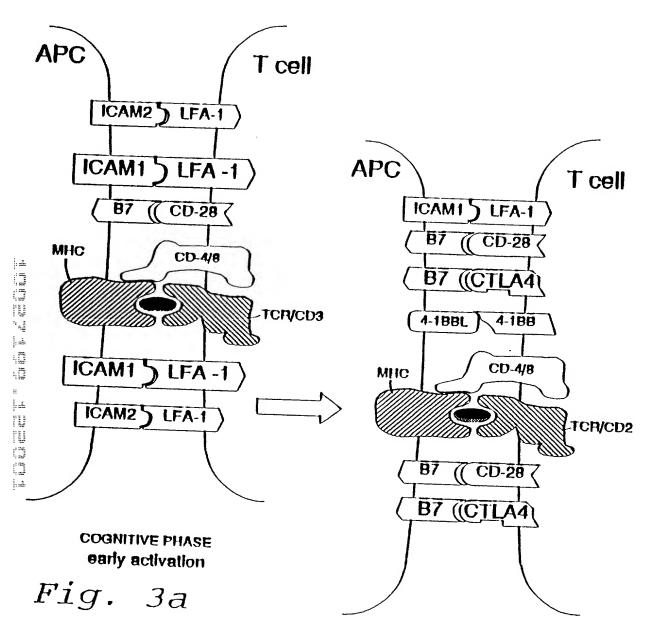
TGC CGA	TGT Cys					GAA Gl u							GAG GI U	785
CTG TGA														771
TGTACTATO CACCATCCT TCATCCTAO	ĪĞ	TAGG/ TGGA/ TGAT(\CAG(CAC	AAGC	CCGA/ AACCC CACCT	: CV	CGAG/ CCAC(FCCA/	CCTG		NGGA0 FTAC/ FCTA/	\CA		821 871 921
CTAACATA1 TATGTGTG1		TGTC1 AGTG1				TAAAT TGTAT		TTTTT ACACO			GTGT			971 021
GTGTGTGAG CCATAAGAA	VC .	CT CC1 TGGAC	STTAT	GG	ATGG	GAGGT CTGTG	AG	SAAG/ CCGGN	INNG	ATAC	STTGG SGTCG	GG	İ	071 121
ACGGAGACO GATATTTCO	G (GT CT T GAAT T	GTAC	A G	ATTG	CGTGA	ACA	STAT/	TCT	AGT1	AAAA OTAA	SAT	1	171 221
CTAAGAGGA ATATGTATA	AT .	TTGTT	SACTO	ŤŤ	TTACI	TACT	AAC	ATATO STCA/	CCT	AGAG	ATAT	CTG	1	271 321 371
ACACACACACACACACACACACACACACACACACACAC	AČ A	CAATT ACGTT GGGTA	TATA	C T	ACGT/	TTTA NCTGT NAAGA	ŤĂĨ	CACA CGGT SAGT	ATT	CTAC	ACAC GTC/ TGTC	NTA	į.	421 471
GGTGACAGA GTCTAAAA	CT (TACCO	TAGA	A G	TCTCC	GTAG STCAA	GT1	CCCC	GAC	GAAG	CGGA AGGA	(CA	1	521 571
GAGGAGACA TCGTGACAC AGGTCAGGT	CT	AGT CO CCACO GT ACO	CCTT	GTO	GGAC/	TTTC \CTTG GCGG	AGT	GT CA GT CA NGACA	TCC	TTGC	CCTC	GΛ	11	621 671 721
GCTACGAGA TTTAATCTC	A C	CGAC CAAGT	TCAC	A GO	GGGG	CCCG	GGC	SACCT	ATG	ATG/ GCGI	CGAT	CC	11	771 821
GGTACTAAT CTTTAAGAA	T	AT CCT CT CCC CT GGC	TGCC	G G	cccc	TAAAA CGTAA CTGGT	GC/	NCCAA NTAAC GCTT	GCG	GCGA	GACT	ĊΛ	1 !	871 921 971
TTACAAAAC ATGGCAGCA	iŤ /	AATTA	GTTC	TTO	CTTT	CAGC	CTC	CAAG	CTT	CTGC	TAGT	CT	20	021 071
AAT AAGGGT AGGCCCCCC	T (CTGGG	CAAC	Ğ TI	TTCG/	AGGC	CCT GAT	TTGG	TTT		AACC		2	121 171
GGTGGGTGC	C 1	TTAGC	ICIT	i Ci	CGAT	AGTT	AGA	(C					22	205

Fig. 2a

human homologue of mouse 4-1bb									
h4-1bb Length 838									
1	AATCAGCTTT	GCTAGTATCA	TACCTGTGCC	AGATTTCATC	ΛΤGGGΛΛΛCΛ				
51	GCTGTTACAA	CATAGTAGCC	ACTCTGTTGC	TGGTCCTCAA	CTTTGAGAGG				
101	ACAAGATCAT	TGCNGGNTCC	TTGTAGTAAC	TGCCCAGCTG	GTACATTCTG				
151	TGATAATAAC	NGGNATCAGA	TTTGCAGTCC	CTGTCCTCCA	AATAGTTTCT				
201	CCAGCGCAGG	TGGNCNNNGG	ACCTGTGACA	TATGCAGGCA	GTGTAAAGGT				
251	GTTTTCAGGA	CCAGGAAGGA	GTGTTCCTCC	<i>ACCAGCAATG</i>	CAGAGTGTGA				
301	CTGCACTCCA	GGGTTTCACT	GCCTGGGGGC	AGGATGCAGC	ATGTGTGAAC				
351	AGGATTGTAA	ACAAGGTCAA	GAACTGACAA	AAAAAGGTTG	TAAAGACTGT				
401	TGCTTTGGGA	CATTTAACGA	TCAGAAACGT	GGCATCTGTC	GACCCTGGAC				
451	ANACTGTTCT		AGTCTGTGCT	TGTGAATGGG	ACGAAGGAGA				
501 551	GGGACGTGGT	CTGTGGACCA	TCTCCAGCTG	ACCTCTCTCC	GGGNGCNTCC				
601	TCTGTGACCC			CCAGGACACT	CTCCGCAGAT				
651	CATCTCCTTC		TGACGTCGAC		TTCCTGCTGT				
701	CTGTATATAT		TCTGTTGTTA		AAAGAAACTC				
751	GGANGATGGC	TCTACCTCCC	ATTATGAGA	CCAGTACAAA	CTACTCAAGA				
801		TCCAACTCAA	TACCCCTCTT	ΛGΛΛGΛΛGΛΛ	GGAGGATGTG				
001	MCIGIGIUM	TGGNAGTCAA	INGGGCTGTT	GGGACTTT					

Fig. 2b

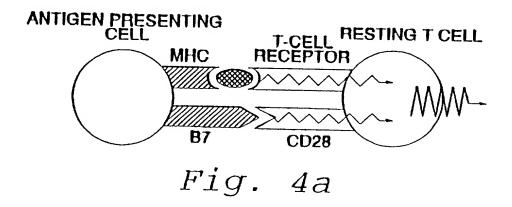
55 60 65 70 75	1 TCTGTGACCC 1 CATCTCCTTC 1 TCTTCCTCAC 1 CTGTATATAT	CTGTGGACCA CGCCTGCCC TTTCTTGCGC GCTCCGTTTC TCAAACAACC TGTAGCTGCC TGGAAGTCAA	TGCGAGAGAG TGACGTCGAC TCTGTTGTTA ATTTATGAGA GATTTCCAGA	CCAGGACACT TGCGTTGCTC AACGGGGCAG CCAGTACAAA AGAAGAAGAA	CTCCGCAGAT TTCCTGCTGT AAAGAAACTC CTACTCAAGA
			ig. 2b		
1 51 101 151 201 251	TKERDVVCGP	TCDICRQCKG ELTKKGCKDC SPADLSPGAS	VFRTRKECSS CFGTFNDQKR SVTPPAPARE	TSNAECDCTP GICRPWTNCS FGHSPOLISE	GFHCLGAGCS LDGKSVLVNG FLALTSTALL

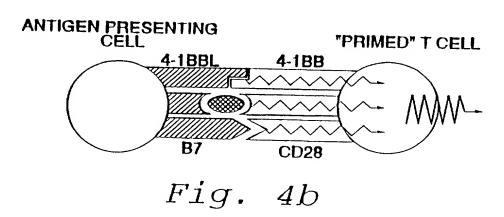


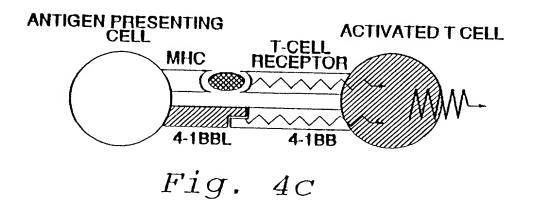
PROLIFERATION CLONAL EXPANSION late activation

Fig. 3b

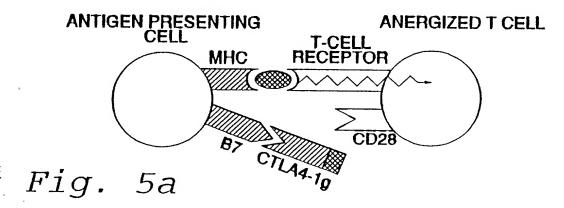
NORMAL T-CELL ACTIVATION PATHWAY







BLOCKING STEPS IN T-CELL ACTIVATION PATHWAY



[-≛

